REMARKS

I. Introduction

Receipt is acknowledged of a final office action dated August 6, 2004. In the action, the examiner rejected claims 30, 33 and 35 as allegedly non-enabled, claims 11, 30-45 and 60-62 as allegedly failing to meet the written description requirement, and claims 11, 31, 32, 34, 36-43 and 60-62 as allegedly anticipated by Ellis et al., *Nature Genetics,* 8:285-290 (1994).

Reconsideration of this application is respectfully requested.

II. Status of the Claims

In this amendment, applicants amended claims 11, 60 and 62. Support for the amended claims can be found throughout the specification, and in originally filed claim 11 in particular. Upon entry of this amendment, claims 11, 30-45 and 60-62 will be under examination.

Because the foregoing amendments do not introduce new matter, entry thereof by the Examiner is respectfully requested.

III. Claims Rejected under 35 U.S.C. § 112, 1st paragraph

A. Enablement Rejection

Claims 30, 33 and 35 were rejected under 35 U.S.C. § 112, first paragraph, as allegedly not enabled. In particular, the claims were rejected because "one of skill in the art would have no way of knowing what diseases or disorders the cell surface glycoprotein with the primary peptide sequence of SEQ ID NO: 1 would be associated with prior to the disclosure of SEQ ID NO: 1 by Applicant in the instant specification" and "the artisan would have no way of knowing what conditions to diagnose because no conditions are disclosed in the instant specification. Applicants respectfully disagree.

As previously provided, applicants respectfully draw the Examiner's attention to Ellis *et al., Nature Genetics*, Vol. 8, November 1994 ("Ellis I"), and Ellis *et al., Nature Genetics,* Vol. 6, April 1994 ("Ellis II") copies of which were submitted to the US PTO with an IDS filed on

November 30. 2001. The Ellis papers explain the importance of XG (formerly PBDX), stating that the XG region maps to the X-specific region adjacent to MIC2 and is therefore a marker for MIC2 (Ellis I, page 289, column 1, paragraph 2). MIC2 exhibits an erythrocyte-specific quantitative polymorphism characterized by either a high or low level of CD99 (Ellis II, page 285, column 1, paragraph 2). Therefore, XG (and the protein of the invention) is a marker for such polymorphisms.

Also, an unusual kind of cis-acting regulation exists (possibly at the transcriptional level) at or near this site which appears to be involved in, and linked to, various sex-linked diseases including Klinefelter's syndrome (Ellis II, page 394, column 1, paragraph 1). These teachings in these references cannot be dismissed.

Further, "The Blood Group Antigen Facts Book," at page 252 explicitly states that the XG blood group system "has helped define the mechanism responsible for various sex-chromosome aneuploides." Considering the degree of sequence similarity between SEQ ID NO:1 and XG, the polypeptide of SEQ ID NO:1 may be used as a marker for the XG blood group in the same way that XG is used. Thus, the Ellis and Antigen Facts Book references demonstrate the clinical significance of SEQ Id NO: 1 as an XG blood group system marker.

For at least these reasons, Applicants' claims are enabled and, therefore, withdrawal of this ground for rejection is respectfully requested.

B. Written Description Rejection

Claims 11, 30-45 and 60-62 were rejected under 35 U.S.C. § 112, first paragraph, as allegedly failing to meet the written description requirement. Specifically, the claims were rejected because "[o]ne of skill in the art would conclude that Applicant was not in possession of the claimed genera of polypeptides comprising a 'naturally occurring amino acid sequence at least 90% identical to the amino acid sequence of SEQ ID NO: 1' and 'biologically active fragments of a polypeptide having the amino acid sequence of SEQ ID NO: 1.'" Office action at 4.

The office action did however provide that "[a] polypeptide comprising the amino acid sequence of SEQ ID NO:1 adequately described in the specification as-filed, thereby providing

adequate written description of an antibody which specifically binds the polypeptide of SEQ ID NO: 1 or immunogenic fragments thereof." Office action at 4. Thus, in the interest of expediting prosecution, applicants amended claim 11 to recite an antibody which specifically binds to a polypeptide consisting of SEQ ID NO: 1 and immunogenic fragments thereof. Applicants trust that this amendment addresses the Office's concerns.

IV. Rejections Under 35 U.S.C. § 102

Claims 11, 31, 32, 34, 36-43 and 60-62 were rejected under 35 U.S.C. § 102(b) as allegedly anticipated by Ellis et al., asserting that "the antibodies of Ellis were made using an immunogenic fragment of PBDX having the amino acid sequence 'QRDFDLADALDDP'" and that "[t]he immunogenic peptide of Ellis is identical to amino acid residues 22-34 of SEQ ID NO: 1." Office action at 6. Therefore, the Office concluded that "the antibodies of Ellis will bind to SEQ ID NO: 1." *Id.* Applicants respectfully traverse this ground for rejection.

Ellis does not teach the claimed invention. Ellis describes making an antibody to a naturally occurring Xg^a blood group antigen, but not an antibody that binds SEQ ID NO: 1 or an immunologically active fragment of SEQ ID NO: 1. The antibody of Ellis was made with an immunogenic fragment that is not 100% identical to a fragment in SEQ ID NO: 1, but in fact contains an additional residue that is not present in SEQ ID NO: 1. Therefore, it is possible that the antibodies of Ellis do not bind SEQ ID NO: 1.

Moreover, the protein in Ellis is 92.3% identical to SEQ ID NO: 1 but the differences in sequence similarity may confer alternative peptide folding of SEQ ID NO: 1. While such sequence differences may not affect function of the two proteins, small variations in the sequences may affect the 3-dimensional conformation of the two proteins. Thus, such conformational differences may render the epitope recognizable by the Ellis antibody inaccessible in the native conformation of the polypeptide of SEQ ID NO: 1.

In fact, "[l]inear determinants [epitopes formed by adjacent amino acid residues in the covalent sequence] may be accessible to antibodies in the active folded protein if they appear on the surface or in a region of extended conformation." Abbas, et al., CELLULAR AND MOLECULAR

IMMUNOLOGY, 2ND ED., (1994) p. 47. As such, it can not be assumed that the antibodies of Ellis will bind SEQ ID NO: 1 of the present invention.

In view of the foregoing arguments, it is respectfully requested that the present rejections be withdrawn.

CONCLUSION

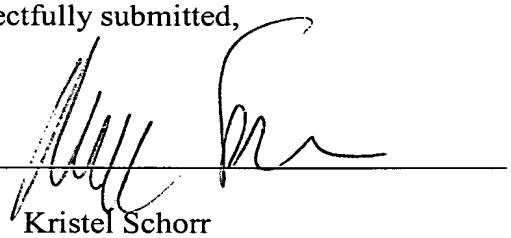
Reconsideration of the present application in view of the foregoing amendments and arguments is kindly requested.

It is respectfully urged that the present application is now in condition for allowance. Early notice to that effect is earnestly solicited.

Examiner Vandervegt is invited to contact the undersigned by telephone if it is felt that a telephone interview would advance the prosecution of the present application

Respectfully submitted,

Date: November 8, 2004

By 

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